



OIPE

ENTERED

## RAW SEQUENCE LISTING

DATE: 06/14/2002

PATENT APPLICATION: US/10/007,489B

TIME: 14:49:25

Input Set : A:\EP.txt

Output Set: N:\CRF3\06142002\J007489B.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Frayne, Elizabeth Gay

7 (ii) TITLE OF INVENTION: Microbial Production of  
8 Nuclease Resistant DNA, RNA, and Oligo Mixtures

10 (iii) NUMBER OF SEQUENCES: 2

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Frayne, Elizabeth Gay

14 (B) STREET: 2027 Galvin Ln. #1

15 (C) CITY: Diamond Bar

16 (D) STATE: California

17 (E) COUNTRY: USA

18 (F) ZIP: 91765

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Diskette, 3.50 inch 1.4 MB

21 (B) COMPUTER: IBM

22 (C) OPERATING SYSTEM: Windows XP

23 (D) SOFTWARE: Microsoft Word

24 (vi) CURRENT APPLICATION DATA:

C--&gt; 25 (A) APPLICATION NUMBER: US/10/007,489B

C--&gt; 26 (B) FILING DATE: 05-Dec-2001

27 (C) CLASSIFICATION:

28 (vii) PRIOR APPLICATION DATA:

29 (A) APPLICATION NUMBER: US 60/100,231

30 (B) FILING DATE: 14-SEP-1998

31 (A) APPLICATION NUMBER: US 60/152,371

32 (B) FILING DATE: 07-SEP-1999

33 (ix) TELECOMMUNICATION INFORMATION:

34 (A) TELEPHONE: (909)861-2111/860-7415

35 (2) INFORMATION FOR SEQ ID NO: 1:

36 (i) SEQUENCE CHARACTERISTICS:

37 (A) LENGTH: 22 base pairs

38 (B) TYPE: nucleic acid

39 (C) STRANDEDNESS: single

40 (D) TOPOLOGY: linear

41 (ii) MOLECULE TYPE: genomic DNA

42 (iii) HYPOTHETICAL: no

43 (iv) ANTI-SENSE: no

44 (vi) ORIGINAL SOURCE:

45 (A) ORGANISM: Saccharomyces cerevisiae

46 (B) STRAIN: YFLO39C genomic clone

47 (x) PUBLICATION INFORMATION:

48 (A) AUTHORS: Murakami Y., Naitou M., Hagiwara H., Shibata T.,

## RAW SEQUENCE LISTING

DATE: 06/14/2002

PATENT APPLICATION: US/10/007,489B

TIME: 14:49:25

Input Set : A:\EP.txt

Output Set: N:\CRF3\06142002\J007489B.raw

49 Ozawa M., Sasanuma S.I., Sasanuma M., Tsuchiya Y., Soeda E.,  
 50 Yokoyama K., Yamazaki M., Tashiro H., Eki T.  
 51 (B) TITLE: Analysis of the nucleotide sequence of chromosome VI from  
 52 *Saccharomyces cerevisiae*.  
 53 (C) JOURNAL: Nature Genet.  
 54 (D) VOLUME: 10  
 55 (F) PAGES: 261-268  
 56 (G) DATE:1995  
 57 (K) RELEVANT RESIDUES IN SEQ ID NO: 1: 10-31  
 58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 59 GAG GTT GCT GCT TTG GTT ATT G 22  
 60 (2) INFORMATION FOR SEQ ID NO: 2:  
 61 (i) SEQUENCE CHARACTERISTICS:  
 62 (A) LENGTH: 22 base pairs  
 63 (B) TYPE: nucleic acid  
 64 (C) STRANDEDNESS: single  
 65 (D) TOPOLOGY: linear  
 66 (ii) MOLECULE TYPE: genomic DNA  
 67 (iii) HYPOTHETICAL: no  
 68 (iv) ANTI-SENSE: yes  
 69 (vi) ORIGINAL SOURCE:  
 70 (A) ORGANISM: *Saccharomyces cerevisiae*  
 71 (B) STRAIN: YFLO39C genomic clone  
 72 (x) PUBLICATION INFORMATION:  
 73 (A) AUTHORS: Murakami Y., Naitou M., Hagiwara H., Shibata T.,  
 74 Ozawa M., Sasanuma S.I., Sasanuma M., Tsuchiya Y., Soeda E.,  
 75 Yokoyama K., Yamazaki M., Tashiro H., Eki T.  
 76 (B) TITLE: Analysis of the nucleotide sequence of  
 77 chromosome VI from *Saccharomyces cerevisiae*.  
 78 (C) JOURNAL: Nature Genet.  
 79 (D) VOLUME: 10  
 80 (F) PAGES: 261-268  
 81 (G) DATE:1995  
 82 (K) RELEVANT RESIDUES IN SEQ ID NO: 2: 1097-1118  
 83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 84 TT GTG GTG AAC GAT AGA TGG AC 22

VERIFICATION SUMMARY

DATE: 06/14/2002

PATENT APPLICATION: US/10/007,489B

TIME: 14:49:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\06142002\J007489B.raw

L:25 M:220 C: Keyword misspelled or invalid format, -[(A) APPLICATION NUMBER:]

L:26 M:220 C: Keyword misspelled or invalid format, -[(B) FILING DATE:]

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Frayne, Elizabeth Gay

(ii) TITLE OF INVENTION: Microbial Production of Nuclease Resistant DNA, RNA, and

Oligo Mixtures

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Frayne, Elizabeth Gay

(B) STREET: 2027 Galvin Ln. #1

(C) CITY: Diamond Bar

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 91765

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch 1.4 MB

(B) COMPUTER: IBM

(C) OPERATING SYSTEM: Windows 98

(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 10/007,489

(B) FILING DATE: 12/05/2001

(C) CLASSIFICATION: 435/41, 435/71, 435/91, 435/131, 435/154, 435/172, 435/183; 935, 536/27

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION (PROVISIONAL) NUMBER: US 60/100,231

(B) FILING DATE: 9/14/98

(C) APPLICATION (PROVISIONAL) NUMBER: 60/152,371

(D) FILING DATE: 9/07/99

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (909)861-2111/860-7415

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANSIM: Saccharomyces cerevisiae

(B) STRAIN: YFLO39C genomic clone

(vi) PUBLICATION INFORMATION:

(A) AUTHORS: MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M., SASANUMA S.I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K., YAMAZAKI M., TASHIRO H., EKI T.

(B) TITLE: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.

(C) JOURNAL: Nature Genet.

RECEIVED

MAR 27 2002

TECH CENTER 1600/2900

RECEIVED

MAR 27 2002

TECH CENTER 1600/2900

(D) VOLUME: 10  
 (C) PAGES: 261-268  
 (D) DATE:1995  
 (E) RELEVANT RESIDUES IN SEQ ID NO: 1: 10-31  
 (vii) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 GAG GTT GCT GCT TTG GTT ATT G  
 (3) INFORMATION FOR SEQ ID NO: 2:  
 (i)SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 bp  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE:  
 (A)DESCRIPTION: genomic DNA  
 (iii) HYPOTHETICAL: no  
 (iv) ANTI-SENSE: yes  
 (v) ORIGINAL SOURCE:  
 (A) ORGANSIM: Saccharomyces cerevisiae  
 (B) STRAIN: YFLO39C genomic clone  
 (vi) PUBLICATION INFORMATION:  
 (A) AUTHORS: AUTHORS: Murakami Y., Naitou M., Hagiwara H., Shibata T.,  
 Ozawa M., Sasanuma S.I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,  
 Yamazaki M., Tashiro H., Eki T.  
 (B) TITLE: Analysis of the nucleotide sequence of chromosome VI from  
 Saccharomyces cerevisiae.  
 (C) JOURNAL: Nature Genet.  
 (D) VOLUME: 10  
 (B) PAGES: 261-268  
 (C) DATE:1995  
 (D) RELEVANT RESIDUES IN SEQ ID NO: 2: 1097-1118  
 (vii) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
 TT GTG GTG AAC GAT AGA TGG AC

10/007,489

pp 1-3

SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

(1) GENERAL INFORMATION

(i) APPLICANT: Elizabeth Frayne

~~(ii) APPLICANT ADDRESS: 2027 Galvin Ln. #1~~

*delete*

(ii) ~~(iii)~~ TITLE OF INVENTION: Microbial Production of  
Nuclease Resistant DNA, RNA, and Oligo Mixtures

(iii) ~~(iv)~~ NUMBER OF SEQUENCES: 2

(iv) ~~(v)~~ CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Frayne Consultants
- (B) STREET: 1249 S. Diamond Bar Blvd. #125
- (C) CITY: Diamond Bar
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 91765

(v) ~~(iv)~~ COMPUTER READABLE FORM

- (A) MEDIUM TYPE: Diskette, 3.50 inch 1.2 KB
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: Windows 98
- (D) SOFTWARE: Microsoft Word

(vi) ~~(vii)~~ CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- ~~(C) CLASSIFICATION: 435/41, 435/71, 435/91,  
435/131, 435/154, 435/172, 435/183, 935,  
536/27~~

*delete*

(vii) ~~(viii)~~ PRIOR APPLICATION DATA:

- (A) APPLICATION ~~(PROVISIONAL)~~ NUMBERS: *current* (A) APPLICATION NUMBER:  
~~unknown, 607/152, 371, 607/100, 231~~
- (B) FILING DATE: ~~current unknown, 9/07/99~~ *07-SEP-1999*  
*use this date format*
- (A) APPLICATION NUMBER: *14-SEP-1999*

(ix) TELECOMMUNICATION INFORMATION: *Colon*

- (A) TELEPHONE: (909) 861-2111/860-7415
- ~~(B) EMAIL: egfrayne@cs.com~~

(2) INFORMATION FOR SEQ ID NO 1:

(i) SEQUENCE CHARACTERISTICS: *Colon*

- (A) LENGTH: 22 bp

*insert colon  
after each  
heading*

*list each prior  
serial number  
separately*

10/007,489 2

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: oligonucleotide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ~~+~~ ORIGINAL SOURCE:

- (A) ~~ORGANSIM~~ ORGANISM Saccharomyces cerevisiae
- (B) STRAIN: YFLO39C genomic clone

Per 1.823  
of sequence  
Rules, list

(x) ~~+~~ PUBLICATION INFORMATION:

- (A) ~~AUTHORS:~~ AUTHORS: Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.

each  
author  
on a  
separate  
line

- (B) TITLE: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.

- (C) JOURNAL: Nature Genet.

- (D) VOLUME: 10

- (F) ~~+~~ PAGES: 261-268

- (G) ~~+~~ DATE: 1995

- (K) ~~+~~ RELEVANT RESIDUES IN SEQ ID NO 1: 10-31

:< colon

(xi) ~~+~~ SEQUENCE DESCRIPTION: SEQ ID NO 1:

delete

(maximum  
of first  
ten authors)

GAGGTTGCTG CTTTGATTAT TG

22

SURNAME ~~comma~~ OTHER NAMES  
and/or  
INITIALS

(2) ~~+~~ INFORMATION FOR SEQ ID NO 2:

T

insert

cumulative

base total at right

margin

of each

line

(i) SEQUENCE CHARACTERISTICS:

- (A) ~~+~~ LENGTH: 22 bp
- (B) ~~+~~ TYPE: nucleic acid
- (C) ~~+~~ STRANDEDNESS: single
- (D) ~~+~~ TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) ~~+~~ DESCRIPTION: oligonucleotide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

→ (vi)

→ ORIGINAL SOURCE:

(A) ~~(F)~~ ORGANSIM: Saccharomyces cerevisiae(B) ~~(G)~~ STRAIN: YFLO39C genomic clone

misspelled

fix format

(X) ~~(vi)~~ PUBLICATION INFORMATION:(A) ~~AUTHORS:~~ AUTHORS: Murakami Y., Naitou M.,  
Hagiwara H., Shibata T., Ozawa M., Sasanuma S.I.,  
Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,  
Yamazaki M., Tashiro H., Eki T.

as

indicated

on

page

2

(B) TITLE: Analysis of the nucleotide sequence of  
chromosome VI from Saccharomyces cerevisiae.

(C) JOURNAL: Nature Genet.

(D) VOLUME: 10

(F) ~~(H)~~ PAGES: 261-268(G) ~~(I)~~ DATE: 1995(K) ~~(J)~~ RELEVANT RESIDUES IN SEQ ID NO: 1: 1097-1118

do you mean 2?

(X) ~~(vii)~~ SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTGTGGTGAA CGATAGATGG AC

22 ← insert

1) Please consult sequenceRules for valid format.2) See sample sequence listing (attached)3) FYI: all U.S. applications filed on or  
after July 1, 1998, and which cannot  
claim a prior invention filed before  
July 1, 1998, need to be in new  
sequence Rules format.